

Run on: March 25, 2005, 23:49:35 ; Search time 7133 Seconds
 (without alignments)
 11473.554 Million cell

updates/sec

Title: US-10-009-643-3
 Perfect score: 1689
 Sequence: 1 taaggaagataaaagaatta.....atactcagtccttcacacaga
 1689

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						

1	487.8	28.9	1629	10	RATGHRHREC	L01407 Rat	
growth							
2	485	28.7	1615	9	HUMGRFREC1	L09237 growth	
horm							
3	485	28.7	1615	11	G31682	G31682	
sWSS1621 Er							
4	484.6	28.7	1272	6	AR068141	AR068141	
Sequence							
5	484.6	28.7	1272	6	I31743	I31743	
Sequence 7							
6	484.6	28.7	1272	6	I38170	I38170	
Sequence 7							
7	484.6	28.7	1272	6	I51134	I51134	

Run on: March 25, 2005, 20:56:47 ; Search time 886 Seconds
 (without alignments)
 11284.925 Million cell

updates/sec

Title: US-10-009-643-3
 Perfect score: 1689
 Sequence: 1 taaggaagataaaagaatta.....atactcagtccttcacacaga
 1689

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	1689	100.0	1689	4	AAA89245		Aaa89245
Chicken g							
2	487.8	28.9	1629	2	AAQ62313		Aaq62313 Rat
somat							
3	487.8	28.9	1629	10	ADB58132		Adb58132
Toxicity-							
4	487.8	28.9	1629	10	ADB52617		Adb52617
Primary r							
5	484.6	28.7	1272	2	AAT47109		Aat47109
Human acr							
6	484.6	28.7	1272	2	AAT77198		Aat77198 HAP
7.3 D							
7	484.6	28.7	1272	2	AAV81456		Aav81456
Human clo							

DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; Hormone_2; 2.
 DR PRINTS; PR00275; GLUCAGON.
 DR PROSITE; PS00260; GLUCAGON; 2.
 KW Alternative splicing; Amidation; Cleavage on pair of basic residues;
 KW Glucagon family; Hormone; Polymorphism; Signal.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 80
 FT PEPTIDE 82 126 Growth hormone-releasing factor.
 FT PEPTIDE 129 166 Pituitary adenylate cyclase activating polypeptide.
 FT PROPEP 170 173
 FT MOD_RES 166 166 Lysine amide (G-167 provides amide group)
 FT (Potential).
 FT VARSPLIC 78 78 G -> S (in isoform Short).
 FT /FTId=VSP_001762.
 FT VARSPLIC 79 113 Missing (in isoform Short).
 FT /FTId=VSP_001763.
 FT VARIANT 22 22 S -> C.
 FT VARIANT 61 61 P -> S.
 FT VARIANT 78 78 G -> R.
 FT VARIANT 122 122 T -> S.
 FT VARIANT 165 165 N -> S.
 FT VARIANT 171 171 G -> A.
 SQ SEQUENCE 173 AA; 19704 MW; 2B0B554F43C738F2 CRC64;

Query Match 87.4%; Score 97; DB 1; Length 173;
 Best Local Similarity 87.0%; Pred. No. 2.8e-07;
 Matches 20; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;

Qy 1 SKAYRKLLGQLSARLYLHSLMAK 23
 :||||| ||||||| |||||||
 Db 88 NKAYRKALGQLSARKYLHSLMAK 110

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				

1	111	100.0	23	4	AAB19982		Aab19982
Chicken g							
2	105	94.6	46	4	AAB19980		Aab19980
Chicken g							
3	104	93.7	29	5	ABP53237		Abp53237
Growth ho							
4	104	93.7	43	2	AAW59861		Aaw59861
Amino aci							
5	104	93.7	46	2	AAW59858		Aaw59858
Amino aci							
6	104	93.7	74	8	ADI61809		Adi61809
Chicken G							
7	104	93.7	172	2	AAW59860		Aaw59860
Alternati							
8	104	93.7	175	2	AAW59857		Aaw59857
Amino aci							
9	97	87.4	29	5	ABP53236		Abp53236
Growth ho							
10	97	87.4	45	2	AAR66188		Aar66188
Sockeye s							
11	97	87.4	173	2	AAR66184		Aar66184
Sockeye s							
12	96	86.5	113	2	AAR66186		Aar66186
Sturgeon							
13	94	84.7	29	1	AAP81747		Aap81747